Scoring table: Description: Perfect Score: Statistics: Database: Post-processing: Tabular output not generated Nmatch Sequence: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. STD Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc. n.a. 49:gnEST1 50:gnEST2 51:gnEST3 52:gnEST4 53:gnEST5
54:gnEST6 55:gnEST7 56:gnEST8 57:gnEST9 58:gnEST10
59:gnEST11 60:gnEST12 61:gnEST13 52:gnEST14 63:gnEST15
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SOURCE

ORGANISM: Homo sapiens cDNA clone 666590 5'.

ACESSION

EST.

ORGANISM: Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 463)

AUTHORS

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

TITLE

JOURNAL

The WashU-Merck EST Project

WashU-Merck EST Project

WashU-Merck EST Project

Washington University School of Medicine

SUMMARIES

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Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further is Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 448.
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/note="Organ: mixed (see below); Vector: pT773D-Pac
/note="Organ: mixed (see below); Vector: pT773D-Pac
/Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/clone="666590"
/clone="1b="Soares NhHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
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filler,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Waterston,R., Williamson,A., Wohldmann,P. and
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Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
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Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M. Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marri Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
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Fax: 314 286 1810
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                            Minoru Ko (Wayne State University).
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/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
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18-FEB-1997;

mp53f02.r1 sc

EST:
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Morris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royally-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:347603 Putative full length read vector to vector length is 108 Seq primer: -28M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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"The WashU-HHMI Mouse EST Project";
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                                                                                  1.4%;
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone_lib="Soares
                                                                                                                                                                                                                                                                                        normalization, an M.Fatima Bonaldo.
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s musculus cDNA clone
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Pred. No. 9.46e-03;
0; Mismatches 9
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mp53f02.rl Soares 2
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1 Similarity 76.9%;
30; Conservative
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
                              g1263754
                                                                            DM36D7S 156 bp
D. melanogaster STS (
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Fax: 314 286 1810
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 sequence tagged site fruit fly.
                                                 270880
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Seq primer: -28M13 rev2 from Amersham.
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/lab_host="DH10B"
<1..>107
a 16 c 24 g
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/clone-"572955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
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Pred. No. 9.46e-03;
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1 (bases 1 to 194)
Gerken, S.C. Matsunami, N., Lawrence, E., Carlson, M., Moore, M.,
Ballard, L., Melis, R., Robertson, M., Bradley, P., Elsner, T.,
Tingey, A., Rodriguez, P., Albertsen, H., Lalouel, J.-M. and White, R.
Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome
Onpublished (1993)
                                                                                                                                                                                                Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: Sts@corona.med.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in_situ_site_primary = 98C
BLASTL_program = BLASTN
database_searched = EMBL
database_version = 45.0 and updates till date_of_search
date_of_search = 08-01-1996
BLAST_program = BLASTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Denaturation: 94C 10sec
Annealing: 58C 10sec
Extension: 72C 20sec
Mg++: 1mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer; STS sequence; microsatellite marker; microsatellite repeat; repeat polymorphism; sequence tagged site.
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Human STS UT5145.
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database_version = 32.0
date_of_search = 15-12-1995.
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clone_name = 36D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-APR-1996) Michael Ashburner, Downing St., Cambridge CB2 3EH, England
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                Initial Denaturation: 94C 300sec PCR Cycles: 5
                                                                                                                                                                Primer A: CTACTCAGGGAGGCAGAC Primer B: ACCAAATCCACTTCACTTAGA
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Similarity 16.2%;
6; Conservative
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                                                                                                                                       32P-label: A Primer
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                                                                                                                          PCR Profile:
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/Strain="Oregon-R"
/Clone="3667"
37 C 30 g 27 t 34
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Pred. No. 9.46e-03;
23; Mismatches 8
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 212)
1 (bases 1 to 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
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/sex="female"
/dev_stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
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63 g 53 t 1 others
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Score 21; DB 12;
Pred. No. 9.46e-03;
0; Mismatches 9
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Pred. No. 9.46e-03;
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Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, Mi Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313tcn@ibm.cl.msu.edu. NCBI g1: 906986
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Eukaryotae; mitochondrial eukaryotae; Viridiplantae;
Eukarophyta; molophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
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12-MAR-1997 (Rel.
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12-MAR-1997 (Rel. 51, Last updated, Version 13)
15616 Arabidopsis thallana cDNA clone 182E10T7.
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Whitehead Institute/MIT Center for Genome Research whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900
                                                                                                                Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                       Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Verrebrata; Gnathostomata; Osteichthyes; Sarcopterygil; Choanata; Tetrapoda; Ammiota; Mammalla; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
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/Clone="182E1077"
/Strain="var columbia"
/note="thale cress"
/72 A; 41 C; 50 G; 70 T;
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S., Thomashow M.,
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REFERENCE
AUTHORS
TITLE
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ACCESSION
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SOURCE
                                                                                                                                                                                                                                                                                              RESULT
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.4%;
Best Local Similarity 70.8%;
Matches 34; Conservative
                                                                                                                                                                                            ORGANISM
                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer_bind
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                                                                                                                                                                                                                                                                                                                                                                       109 tncttgaaatgttacctcatttaaaaaaaacccattttgactcctttt 156
                                                                                                                                                                                                                                                                                                                                                        519 TGCTTTAGATGACGTCTCATTTGAGAAGAACCCATCTGGACATCTTTT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 mM
pH: 9.3
                                                                                                                                                                                                                                                              253
human STS WI-6406.
G06067
                                                                                                                                                                                                              9859312
STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST
Contact: Thomas Hudson Whitehead Institute/MIT Whitehead Institute for
                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prepared with primer pairs derived 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer B: AAAGGAGTCAAAATGGGTTTTT
STS size: 100
                                                                        Mapped
                                                                                      Whitehead Institute/MIT
                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                           collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: thudson@genome.wi.mit.edu
                                                                                                                                  Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.0
Total Vol: 20 ul
                                                                                                                    (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 617
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Annealing: 56 degrees
Polymerization:
PCR Cycles: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermal Cycler:
                                                                        ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="791_B_4; {
963_G_6"
56..80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="791_B_4; 816_F_6; 921_C_9; 963_G_6" complement(134..155) /map="791_B_4; 816_F_6; 921_C_9; 963_G_6" 87 t a 28 c 35 g 87 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
56..155
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Pred. No. 9.46e-03;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 g
   Center for Genome Research
Biomedical Research
                                                                                         Center
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                                                                                         Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 928_A_7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               928_A_7; 934_F_6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         928_A_7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 others
                                                                                       Research;
                                                                                                                                                                                                                        and
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                                                                                       Physically
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                                                                                                                                                                                                                                                                                                                                    Query Match 1.4%;
Best Local Similarity 78.4%;
Matches 29; Conservative
Marra M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin ù Morris M., Schellenberg K., Steptoe M., Tan F., Underwood Moore B., Theising B., Wylie T., Lennon G., Soares B., Wil Waterston R.;
                                                                                                                                                                                                                                 LT 14
MM5835
                                                                                                                                                    29-kpr-1996 (Rel. 47, Created)
03-mAR-1997 (Rel. 5), Last updated, Version 2)
ma38f10.rl Soares mouse p3NMF19.5 Mus musculus
similar to gb:219554 VIMENTIN (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STS
                                                                                                  Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                       W10583;
                                                                                                                                                                                                                                                                                                                                                                                                                                         primer_bind
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                                                                 1-267
                                                                                                                                                                                                                                                                                   774 ACACAGCTCACAAGAACAGACTTTCCAGCTGCTGAAG 810
                                                                                                                                                                                                                                                                                                 123 acacageteacatgtacagacaataaaaactgeteaag 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prepared with primer pairs de Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer A: CATTTGCTTTCATACATACAGTTCC Primer B: CACAGTTGTGAAGCCGTGC STS size: 225
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 Cambridge Center,
Tel: 617 252 1900
Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.0
Total Vol: 20 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCL: 10 m
                                                                                                                                                                                                                                 standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pH: 9.3
                                                                                                                                                                                                                                                                                                                                                                                                     76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denaturation: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymerization:
PCR Cycles: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presoak:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group"
                                                                                                                                                                                                                                                                                                                                                                                                                         group"
complement(235..253)
/map="923_H_8; 959_F_5; 441.7
                                                                                                                                                                                                                                                                                                                                                                                                                group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="923_H_8; 959_F_5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="923_H_8; 959_F_5;
                                                                                                                                                                                                                                                                                                                                                                                                     57 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            롡
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 degrees
                                                                                                                                                                                                                                 EST;
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                                                                                                                                                                                                                                                                                                                                    Score 21; DB 38;
Pred. No. 9.46e-03;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                 49 g
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              G., Soares B., Wilson
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                                      Martin J.,
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                                                                                                                                                                   clone 313003
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                                                                                                     Murinae;
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RESULT
ID MA
AC AJ
NI 91
DT 06
DT 11
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Best Local :
  Contact: Marra M/Mouse EST Project WashID-HHMI Mouse EST Project WashIngton University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@vatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@tmage.llnl.gov) for further information. MGI: 01927 Putative full length read vector to vector length is 295 Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MM1157384
AA239461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-1997 (Rel. 51, Created)
15-MAR-1997 (Rel. 51, Last updated, Version 2)
mv25d08.r1 GuayWoodford Beier mouse kidney day 0 Mus musculus cDNA
clone 656079 5' similar to TR:G497940 G497940 MAJOR VAULT PROTEIN.
                                                                                                                                                                                                                                                         Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST project Washlugton University School of Medicinep 4444 Forest Park Parkway, Washlugton University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Putative full length read Seq primer: ETPrimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The WashU-HHMI Mouse EST Unpublished.
Contact: Marra M/Mouse EST
                                                                                                                                                                                          "The WashU-HHMI Mouse EST Project"; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                           Waterston R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.48;
Similarity 75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP;
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78 A; 70 C; 61 G; 58 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minoru Ko (Wayne State University)."
/clone="313003"
/clone_lib" Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DHIOB (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 95;
Pred. No. 5.47e-04;
0; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
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Best Local S
Matches 2
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                148 tgggccccggaaccatcagggacttggctgtggcgg 183
                                                             y Match 1.4%;
Local Similarity 80.6%;
hes 29; Conservative
43 TGGTCCCCGGAAACCTCAGGGGCTTGGAGGCGGCGG
                                                                                                                               281
                                                                                                                             BP;
                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/strain="C57BL/6J"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTTTT3' Library provided Lisa
                                                                                                                                                                                                                           Guay-Woodford
                                                                                                                          69 A; 75 C; 90 G; 47 T; 0 other;
                                                                                                                                                         /clone_lib="GuayWoodford Beier mouse kidney day
/dev_stage="newborn (day 0)"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                          /clone-"656079"
                                                            Score 22; DB 92;
Pred. No. 5.47e-04;
0; Mismatches 7
                                                                                             Length
                                                               Indels
                                                               0
                                                               Gaps
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Search completed: Thu Aug Job time : 773 secs. 21 10:48:17 1997